

SEQUENCE LISTING

<110> STRYKER CORPORATION

<120> REPAIR OF LARYNX, TRACHEA, AND OTHER FIBROCARTILAGINOUS TISSUES

<130> STK-070 PCT

<140> PCT/US99/17222

<141> 1999-07-30

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1822

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

52223 (49) (1341)

5400>1

ggtgcgggcc cgagccccgg agcccggtta gcgcgttagag ccggcgcg atg cac gtg 57
Met His Val
1

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cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
      5           10           15

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ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
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gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
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cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
 55 60 65

ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
 70 75 80

ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc 345
 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
 85 90 95

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ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
100          105          110          115

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ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac	441
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp	
120 125 130	
atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc	489
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe	
135 140 145	
cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc	537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile	
150 155 160	
cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac	585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
165 170 175	
tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat	633
Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr	
180 185 190 195	
cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc	681
Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu	
200 205 210	
gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac	729
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp	
215 220 225	
atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg	777
Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu	
230 235 240	
ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc	825
Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro	
245 250 255	
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc	873
Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro	
260 265 270 275	
ttc atg gtg gct ttc aag gcc acg gag gtc cac ttc cgc agc atc	921
Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile	
280 285 290	
cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc	969
Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro	
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aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc	1017
Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser	
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agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc	1065
Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
325 330 335	

020203002 - 04006001

cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc	1113
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
340 345 350 355	
gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg	1161
Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
360 365 370	
aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac	1209
Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
375 380 385	
ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc	1257
Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
390 395 400	
atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa	1305
Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
405 410 415	
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Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
420 425 430	
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 <212> PRT
 <213> Homo sapiens

<400> 2
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 1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60

09628607-040601

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365

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Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
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<210> 3

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: OPX

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 3

Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
 1 5 10 15

Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 20 25 30

Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 50 55 60

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 65 70 75 80

Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
 85 90 95

Xaa Ala Cys Gly Cys His
 100

<210> 4

<211> 97

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Generic-Seq-7

09626602-074002

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 4

Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Cys Cys Xaa Pro
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
 85 90 95

Xaa

<210> 5

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Generic-Seq-8

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 5

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
 20 25 30

Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
 35 40 45

Xaa
 50 55 60

Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
 65 70 75 80

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Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
 85 90 95

Xaa Xaa Cys Xaa Cys Xaa
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<210> 6
 <211> 97
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Generic-Seq-9

<220>
 <223> each Xaa is independently selected from a group of one
 or more specified amino acids as defined in the
 specification.

<400> 6
 Xaa
 1 5 10 15

Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa
 20 25 30

Xaa
 35 40 45

Xaa Cys Xaa Pro
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Cys Xaa Cys
 85 90 95

Xaa

<210> 7
 <211> 102
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Generic-Seq-10

<220>
 <223> each Xaa is independently selected from a group of one
 or more specified amino acids as defined in the
 specification.

09626502 044604

<400> 7

Cys	Xaa												
1													15

Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Gly
					20						30		

Xaa	Cys	Xaa											
	35												45

Xaa													
	50												60

Xaa	Xaa	Cys	Xaa	Pro	Xaa								
	65			70									80

Xaa													
													95

Xaa	Xaa	Cys	Xaa	Cys	Xaa
		100			

<210> 8

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative sequence

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 8

Cys	Xaa	Xaa	Xaa	Xaa
1				5

<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative sequence

<220>

<223> each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

<400> 9

Cys	Xaa	Xaa	Xaa	Xaa
1				5